



A systematic review and meta-analysis of bovine tuberculosis occurrence and burden in Bangladesh, 1970–2023

Review

Cite this article: Islam SS, Pateras K, Kabir SML, Kostoulas P, Ward MP and Rahman AKMA (2024). A systematic review and meta-analysis of bovine tuberculosis occurrence and burden in Bangladesh, 1970–2023. *Epidemiology and Infection*, **152**, e126, 1–9
<https://doi.org/10.1017/S0950268824001328>

Received: 15 January 2024

Revised: 11 July 2024

Accepted: 12 July 2024

Keywords:

Mycobacterium bovis; *Mycobacterium orygis*; one health; true prevalence; zoonotic tuberculosis

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Abstract

We aimed to estimate the overall apparent prevalence, true prevalence, and the spatial, temporal, and test-specific burden of bovine tuberculosis in Bangladesh. PubMed, Web of Science, Scopus, Google Scholar, and BanglaJOL were searched for bovine tuberculosis publications in Bangladesh from 1 January 1970 to 23 June 2023. Of 142 articles screened, systematic review and meta-analysis were performed on 22 (15.5%) articles. The apparent estimated bovine tuberculosis prevalence was 7%. The apparent Bayesian pooled mean bovine tuberculosis prevalences based on caudal fold test and single intradermal comparative tuberculin test were 7.83% and 9.89%, respectively, and the true pooled mean prevalences were 10.39% and 10.48%, respectively. Targeted interventions are recommended for districts with higher prevalence to effectively reduce the bovine tuberculosis burden in those areas. Current diagnostic practices employed in Bangladesh may not accurately reflect the bovine tuberculosis burden. Our findings highlight the need for better diagnostic tools and supplemental testing methods to ensure accurate diagnosis and surveillance. Efforts should prioritize obtaining ‘true’ prevalence estimates corrected for misclassification bias, rather than relying solely on apparent prevalence. Underestimating the bovine tuberculosis burden could result in inadequate resource allocation and hinder the implementation of effective control measures.

Introduction

Tuberculosis (TB) is an important disease caused primarily by *Mycobacterium tuberculosis* (*M. tuberculosis*), a distinct member of the *M. tuberculosis* complex (MTBC). It was estimated in 2020 to cause >1.3 million deaths globally, mainly in low- and middle-income countries (LMICs) [1]. Zoonotic TB in cattle – known as bovine tuberculosis (bTB) – poses a considerable burden on animal health and welfare, particularly in endemic settings, which mainly occurs within LMICs. It is estimated that >50 million cattle are infected globally at an annual economic loss of \$3 billion [2]. The causative agent of bTB is *M. bovis*. However, *Mycobacterium caprae* accounts for some of the burden to a smaller extent as a member of the MTBC [3, 4]. Also, *Mycobacterium orygis* has been documented as a causal agent of TB both in animals and humans in some geographical locations, such as South Asia [5]. In addition, *M. tuberculosis*, which belongs to the MTBC, is the etiological agent of human TB. It can cause accidental infection as a reverse zoonosis in animals in close vicinity to infected humans, particularly in regions where human TB is highly prevalent [6, 7]. The hypothesis of reverse zoonosis in densely populated regions has been supported by several epidemiological studies, which confirmed the genetic similarity between the strains of *M. tuberculosis* of animal and human origin [6, 8]. *M. orygis*, an oryx bacillus, has been proposed as a subspecies of MTBC. It was initially misidentified as *M. africanum* from postmortem samples of four Friesian cross-bred dairy cows in Bangladesh using spoligotyping [9]. However, the interpretation was later corrected, revealing that these isolates were *M. orygis*. Between 2008 and 2010, postmortem samples from eighteen cows and two zoo monkeys were confirmed to contain *M. orygis* through conventional and advanced molecular assays [5, 10]. Similarly, *M. orygis* strains were recently isolated from postmortem samples of farmed cattle [5] and captive wild animals – including spotted deer, impala, common eland, wildebeest, and giraffe – from the same geographical locations in Bangladesh [11].

The presence of multiple *Mycobacterium* species can pose challenges for accurate diagnosis. Conventional diagnostic tests do not always distinguish between different *Mycobacterium* species, leading to potential misclassification or underestimation of disease burden.

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Consequently, there is a need for improved diagnostic tools capable of accurately detecting and differentiating between various Mycobacterium species to facilitate targeted control measures.

Moreover, the potential for interspecies transmission and spill-over events between wildlife, domestic animals, and humans further complicates the epidemiological landscape [12].

Prevalence assessments of bTB caused by *M. bovis* are typically based on limited surveys in LMICs. However, comprehensive research on bTB at various geographical locations with representative sample sizes is essential for obtaining a more accurate understanding of the disease's epidemiology, transmission dynamics, and impact on both animal and human populations [13]. Most developed countries have effectively controlled bTB through the implementation of national control programmes. However, achieving a bTB-free status and eradicating the disease remains challenging due to the risk of transmission from wildlife reservoir species to domestic animals. The test and slaughter strategy, a key component of bTB control programmes, has been successfully implemented in many developed nations [14]. This strategy has greatly reduced the burden of *M. bovis* in cattle, resulting in substantial improvement in human health and generating returns on investment in livestock production that are more than ten times the initial cost [15]. In addition to the substantial economic and food security issues posed by bTB, the disease also presents transboundary challenges due to the movement of animals [16].

In Bangladesh, livestock rearing has shifted from extensive to intensive systems over the last several decades. The country's livestock population consists of 24.5 million cattle, 1.5 million buffalo, 26.6 million goats, and 3.6 million sheep [17]. Twenty per cent of rural Bangladeshis directly – and another 50% indirectly – depend on livestock for food security and livelihoods. The contribution of the livestock sector to the national economy was 1.90% in 2021–2022 and the sector is projected to grow at a rate of 3.90% per annum [17]. The national cattle herd in Bangladesh comprises 85% native cattle and 15% cross-bred high-yielding cattle [18]. Native cattle are not sufficient to fulfill the country's requirement for meat and milk due to low efficiency. Thus, artificial insemination (AI) has been used for several decades as part of breeding programmes with proven high-yielding exotic breeds (usually Holstein-Friesian, Jersey, and Shahiwal cross-breeds) to improve the productivity of indigenous cattle in Bangladesh, leading to a steady increase in the number of cross-bred cattle [19]. This change has increased the risk of bTB in cross-bred cattle, since they are more susceptible to the disease compared to indigenous cattle [20].

To the best of our knowledge, no systematic review and meta-analysis on zoonotic TB have been conducted in Bangladesh. The systematic review reported here follows the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement: an updated guideline for reporting systematic reviews [21]. It focuses on the overall apparent prevalence, corrected for misclassification bias 'true' prevalence, and spatial, temporal, and test-specific burden of bTB in Bangladesh. Apparent prevalence refers to the proportion of animals within a population that test positive for a disease using diagnostic tests. It represents the observed prevalence based on the results of these tests. In contrast, true prevalence is the actual proportion of animals in a population that is diseased, regardless of the test results. True prevalence provides a more accurate estimate of the disease burden, considering both true positive and false negative cases. This is done by considering the sensitivity and specificity of the diagnostic tests used. Sensitivity refers to the ability of a test to

correctly identify animals with the disease (few false negative test results), while specificity refers to the ability of the test to correctly identify animals without the disease (few false positive test results).

The absence of a bTB control programme in Bangladesh [22] creates a substantial risk of infection and transmission. The endemic presence of *M. bovis* in Bangladesh poses a considerable challenge, particularly given its potential implications for food security and other associated costs. Compounded by resource limitations, there is a noticeable gap in government investment in disease control measures. To effectively tackle this issue, it is imperative to engage diverse stakeholders, including the livestock farmer, private sector, breeding societies, and civil society. By encouraging collaboration among these entities, we can develop comprehensive strategies aimed at mitigating the impact of *M. bovis*. This collective effort will not only safeguard a crucial national resource but also strengthen food security and yield significant socio-economic benefits.

Materials and methods

This meta-analysis was conducted following the updated PRISMA guidelines [21]. The protocol that outlines the methodology for conducting this systematic review and meta-analysis was submitted to the Open Science Framework (<https://doi.org/10.17605/OSF.IO/5F8HA>).

Search strategy

On 23 June 2023, we conducted a comprehensive literature search of three databases – PubMed, Web of Science, and Scopus – without any language restrictions to identify relevant articles on zoonotic bTB in Bangladesh. Additionally, to ensure a comprehensive search, we retrieved relevant peer-reviewed articles from Google Scholar and BanglaJOL (a database for Bangladeshi journal-published articles) database searches to include any additional articles that were not found in our primary searches. We used the following search terms to identify relevant publications: [*'mycobacterium bovis'* OR tuberculosis OR Tb OR TB] AND (zoonotic) AND (cow OR cattle OR bovine OR buffalo OR sheep or goats) AND (prevalence OR incidence OR risk OR study) AND (Bangladesh)]. We used the EndNote X8 reference manager (Thomson Reuters, Philadelphia, PA USA) to organize and manage all relevant articles, ensuring that duplicate records were eliminated.

Selection criteria

Inclusion criteria

We considered peer-reviewed articles written in English that were published from January 1970 until June 2023 for evaluation. Studies that met all of the following criteria were included in this review and meta-analysis: (a) diagnosis of bovine or zoonotic TB within a cross-sectional study using tuberculin test or rapid test or smear microscopy or Enzyme-Linked Immunosorbent Assay (ELISA) or polymerase chain reaction (PCR) or culture, using tissue samples including lung, liver, and lymph nodes for the diagnosis of bTB; (b) research conducted in Bangladesh; (c) studies conducted in livestock (cattle, buffalo, sheep, and goats); (d) published the prevalence of tuberculosis and the total number of animals surveyed (numerator and denominator values); (e) availability of the full text. We also considered review articles so as to examine their reference lists for potential inclusions.

Exclusion criteria

The peer-reviewed articles were excluded if they: (a) had the incorrect study design (not an epidemiological study, animals selected based on clinical signs); (b) were not available in full-text; (c) lacked essential details such as the study unit, study location, or prevalence data; (d) solely reported genetic characterization; and (e) were not in English.

Data extraction and evaluation

The first and corresponding authors reviewed the selected articles, documents, and reports that were informative and eligible for this research, as shown in Figure 1. Prior to commencing data extraction, a standardized template was generated. This template incorporated population demographics and other associated factors observed in bTB studies, to allow assessment of homogeneity across the bTB prevalence studies. For studies on bTB in cattle including other animal species (buffalo, sheep, and goats) the following information was retrieved: author(s) with study year/year published, study location/districts, type of animal, samples taken, criteria for positivity, sample size, prevalence (%), screening tests, and laboratory evaluation procedures.

Data analysis

Prevalences were estimated from raw proportions and corresponding 95% confidence intervals (CIs) were also calculated. Additionally, variances of the raw proportions were determined. The prevalence data were pooled using a random-effects (RE) model

[23]. The analysis was performed using the ‘meta’ package in R (version 4.2.0), which provides functions for conducting meta-analysis. For the pooled data, the I^2 statistic was used to assess the degree of heterogeneity among the studies included. Additionally, publication bias was explored using methods proposed by [24, 25]. Small-study effects were assessed through the applied sensitivity analyses. Forest plots were produced showing prevalence estimates with their corresponding 95% CIs for each study alongside their overall RE pooled prevalence estimate. Additional sources of heterogeneity were further explored either by visual inspection of the data, forest plots and bias assessment plots, or through meta-regression analyses. Univariate analyses were performed to test the association of selected covariates (subgroups), including time period (year continuous, pre-2015, 2015 and after), farm locations (districts), and screening tests (caudal fold test (CFT), single intradermal comparative tuberculin test (SICTT), Test kits, and other: PCR and ELISA), with the overall estimates. Then, a sensitivity analysis was performed using the leave-one-out approach.

As a second step, we applied a Bayesian hierarchical beta-binomial model to confirm the above results of apparent prevalence estimates and to estimate the true prevalences of bTB. This model accounts for the sensitivities and specificities of the two diagnostic tests used, namely CFT and SICTT tests (tPRiors) [26]. tPRiors is a free web-based application that facilitates the use of Bayesian prevalence methods by non-experts. We assumed that the mean reported sensitivity and specificity of the CFT were 80% and 90%, respectively, with 95% confidence that these are higher than 51% and 80%, respectively [27–32]. We assumed that the mean reported sensitivity and specificity of the SICTT were 53% and 97%,

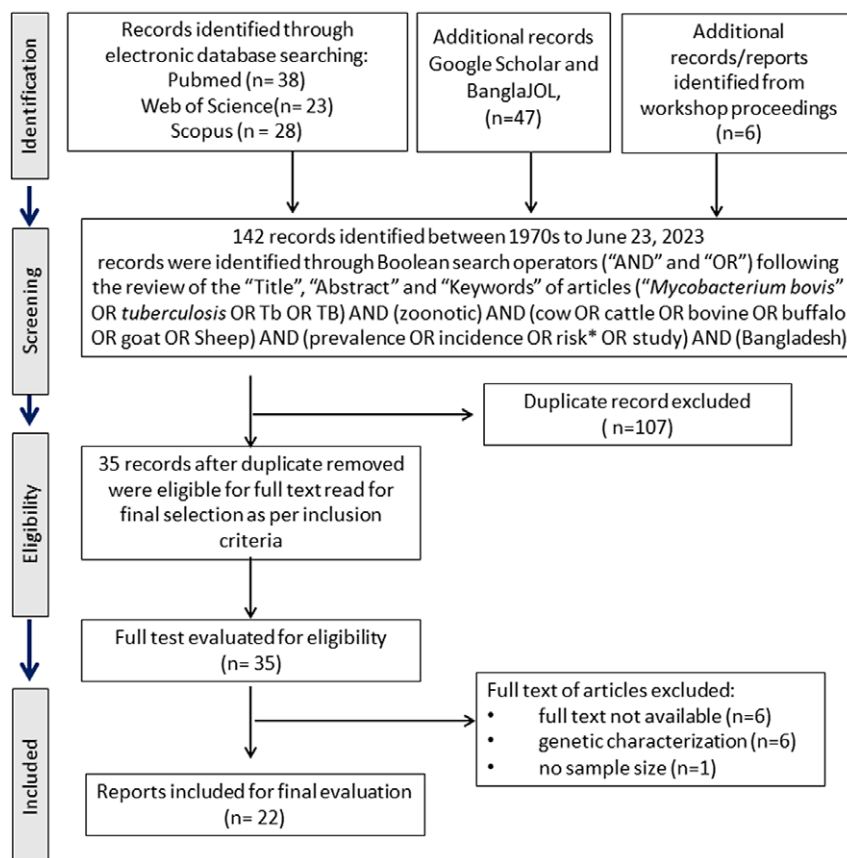


Figure 1. The search and selection strategy applied in a study of bovine tuberculosis occurrence and burden in Bangladesh, 1970–2023 [21].

respectively, with 95% certainty that these are higher than 46% and 94%, respectively [27–32]. Based on this information, we elicited priors on the prevalence using the PriorGen [33]. A sensitivity analysis was performed on the Bayesian model with small prior changes to assess the model's robustness. Such analyses are commonly conducted in the Bayesian framework [34].

Results

Characteristics of targeted studies

Initially, 142 articles with an abstract or summary were identified for review. After screening based on specific inclusion criteria, 35 articles were further evaluated; of these 35 articles, 22 were included for in-depth evaluation (Figure 1, Table 1). The 22 studies included in this analysis collectively contributed bTB prevalence data from a sample size of 8,319 animals, comprising 7,662 cattle, 229 buffaloes, 273 sheep, and 155 goats (Table 1). The studies included in this analysis employed commonly used diagnostic techniques for detecting bTB in animals, such as SICTT, CFT, bTB antibody test kits, polymerase chain reaction (PCR), and enzyme-linked immunosorbent assay. Most diagnostic systems used the CFT as the initial screening test, followed by the application of the comparative cervical tuberculin (CCT) test to confirm the status of

bTB reactor animals. The SICTT and CCT were performed according to standard procedures: an animal was classified as a reactor when the difference in skin thickness increase at the bovine tuberculin injection site was greater than 4 mm compared to the skin thickness increase at the avian tuberculin injection site.

Meta-analysis

Apparent prevalence

Overall, the apparent prevalence was estimated to be 7% (95% CI, 5–10%), with prediction intervals ranging from 1% to 33%. The wide prediction intervals were mostly due to the inclusion of three studies that reported a very high prevalence (27.5, 30 and 33.73%; Figure 2). Subgroup analysis resulted in comparable results between the applied tests, years of study conducted, animal species, and breeds (Supplementary Figures S1–S4). A large difference in prevalence estimates was observed between all districts compared to the Rangpur district, which consisted of only one study with a reported prevalence of 33.73% (Figure 3, Supplementary Figure S5). In studies reported after 2015, the prevalence was 2% lower than those reported prior to 2015 (Supplementary Figure S1). However, this difference was not statistically significant and was mostly influenced by the inclusion of three studies with very large prevalences reported prior to 2015. The diagnostic test had a small impact on

Table 1. Bovine tuberculosis (bTB) prevalence studies in Bangladesh included within a systematic review and meta-analysis, 1970–2023

Study districts	Species	Sample size	Reported prevalence (%)	Screening test	Reference
Mymensingh, Sylhet, Tangail	Cross-bred cattle	289	5.54	CFT	[35]
Mymensingh, Sylhet, Tangail	Indigenous cattle	1,024	2.34	CFT	[35]
Dhaka	Cross-bred cattle	137	27.5	SICTT	[36]
Mymensingh	Indigenous cattle	30	30	bTB Ab Test Kit	[37]
Dhaka	Buffalo	49	6.12	CFT	[38]
Sirajganj	Cross-bred cattle	270	7.78	bTB Ab Test Kit	[39]
Dhaka	Ovine (sheep)	273	9.15	SICTT	[40]
Dhaka	Caprine (goat)	155	1.29	SICTT	[40]
Mymensingh	Both cross-bred and indigenous	101	5.9	TB Ab test kit	[41]
Rangpur	Both cross-bred and indigenous	150	33.73	CFT	[42]
Chattogram	Indigenous cattle	123	11.38	bTB Ab Test Kit	[43]
Dhaka, Sylhet, Bogra, Sirajganj, Mymensingh and Tangail	Cross-bred cattle	696	3.3	SICTT	[44]
Sylhet and Dhaka	Cross-bred cattle	300	12.33	PCR	[45]
Mymensingh	Both cross-bred and indigenous	649	2.34	SICTT	[46]
Mymensingh	Cross-bred cattle	100	5	CFT	[47]
Mymensingh	Cross-bred cattle	100	5	SICTT	[48]
Dhaka	Both cross-bred and indigenous	183	7.1	SICTT	[49]
Chattogram	Cross-bred cattle	846	13.71	CFT	[50]
Chattogram	Cross-bred cattle	289	5.88	ELISA	[51]
Dhaka, Mymensingh, Gazipur, Munshiganj and Jamalpur	Cross-bred cattle	1865	11.3	SICTT	[22]
Mymensingh	Both cross-bred and indigenous cattle	510	7.3	SICTT	[20]
Bhola	Buffaloes	180	3.33	CFT	[52]

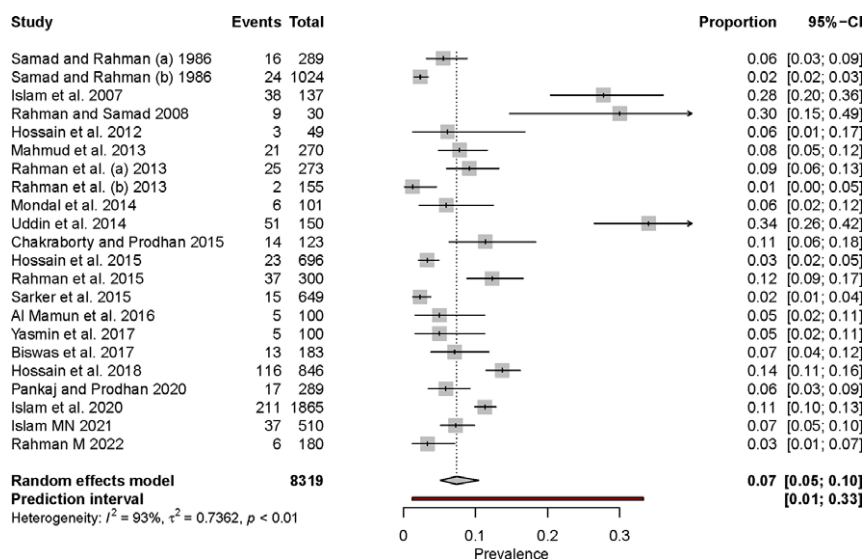


Figure 2. A forest plot represents the reported prevalences of bTB in each publication included in the meta-analysis for this study. The random-effects (RE) models have assigned weights to each publication proportional to sample size to enable a comprehensive comparison of the data. In this context, 'Total' represents the total number of animals included in each publication, while 'Events' refers to the number of animals that tested positive for bovine tuberculosis (bTB). The term 'Proportion' indicates the reported prevalence of bTB within each individual publication.

the prevalence estimates, but the difference was not found to be significant (Supplementary Figure S2). No significant differences were identified in the subgroup analysis among animal species. However, the overall mean prevalence for cattle (8%; 95% CI 6%–12%) was found to be 4% higher compared to other species (4%; 95% CI 2–9%) (Supplementary Figure S3). Similarly, in the subgroup analysis of animal breeds, the mean prevalence of bTB was found to be comparable across different groups: 6% (95% CI: 3–12%) in indigenous cattle, 8% (95% CI: 6–12%) in cross-bred cattle, and 8% (95% CI: 3–17%) in both indigenous and cross-bred cattle (Supplementary Figure S4).

Meta-regression and publication bias assessment

The univariate models showed no significant association that could further explain the between-study variance. To explore potential sources of heterogeneity, meta-regression was implemented with single covariates, including year (both in continuous and categorical forms), sample size, districts (excluding the Rangpur study), and diagnostic tests. None of these covariates were found to have a significant association with the prevalence estimates. The leave-one-out analysis showed robust results with only a 5% change in prevalence estimates when specific studies were excluded. This translated to less than 0.01 of an absolute overall prevalence change (Supplementary Figure S6). Furthermore, the funnel plots indicated an over-representation of mid-sized studies, while many smaller studies were missing, which is common in prevalence-type studies. Nevertheless, based on visual inspection and the application of statistical tests, no specific issues regarding publication bias were identified.

True prevalence

The true pooled mean prevalence of bTB based on CFT and SICTT screening tests was estimated to be 10.39% and 10.48%, respectively, according to tPRiors. However, the apparent Bayesian pooled mean bTB prevalences for the same subgroups of studies were estimated to be 7.83% and 9.89%, respectively. Studies with higher

prevalence when corrected for misclassification bias through the Bayesian model tended to produce even higher prevalences, while studies with lower prevalence tended to produce lower prevalences after correction (Figure 4). The results of the sensitivity analysis (assuming lower prior true prevalence) showed minor fluctuations in the posterior prevalences of bTB (Supplementary Figure S7).

Discussion

Our meta-analysis reveals considerable variability in bTB prevalence estimates across different districts and studies in Bangladesh. We recommend targeted interventions in districts with higher prevalence to effectively combat bTB. Current diagnostic practices in Bangladesh, primarily using CFT and SICTT as screening tests, might not accurately reflect the bTB burden. It is crucial to estimate true prevalence rather than apparent prevalence to accurately measure the actual TB burden in Bangladesh. Underestimating the burden could lead to inadequate resource allocation and hinder the implementation of effective control measures.

The overall estimated bTB prevalence was 7% (95% CI 5–10%) using a RE model. This aligns with a study from India, which reported a prevalence of 7.3% [53]. These findings underscore the urgency for enhanced surveillance and control, especially given the burgeoning domestic livestock sector in Bangladesh. The lack of emphasis on implementing control measures in LMICs, including in Bangladesh [54], is a contributing factor to the high prevalence of bTB. The government carries out bTB screening initiatives primarily in public farms, but with limited outreach to private farms [19].

The national cattle herd in Bangladesh consists of 15% cross-bred cattle and 85% indigenous nondescript cattle [18]. Historically, Bangladesh met its meat demand via cattle imports from India. However, an embargo by the Indian government prompted Bangladesh to focus on domestic livestock production. This led to a surge in cattle farms, from 37,000 in 2011 to >500,000 in 2017, and by 2018 Bangladesh produced a surplus of meat. Consequently, Bangladesh successfully met its national meat demand (including

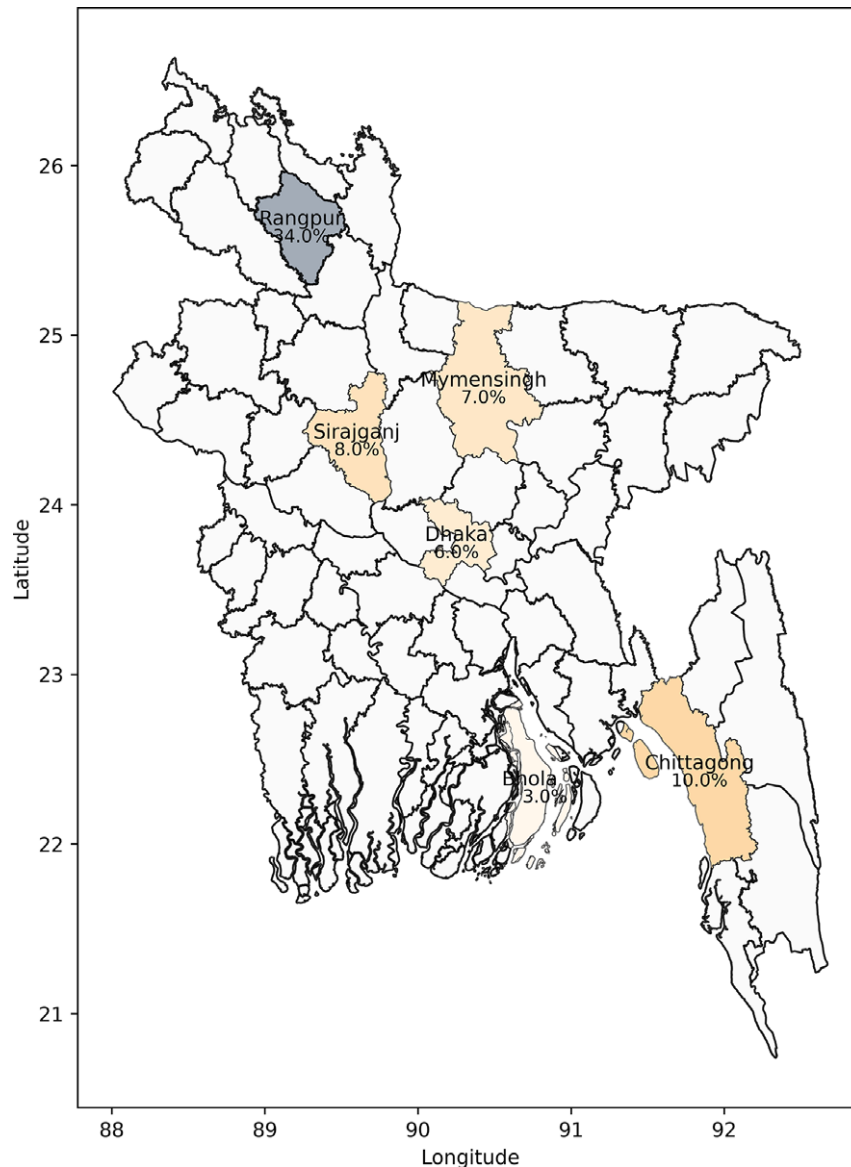


Figure 3. A map showing the study locations and meta-analytic prevalence of bovine tuberculosis in Bangladesh, 1970 to 2023. Produced in Python using Matplotlib and Geopandas libraries.

beef and chicken) in 2018 by producing 7.26 million Metric Tons (MT) of meat, which slightly exceeded the demand of 7.21 million MT [55]. With the steady rise in the number of cross-bred cattle in Bangladesh, the prevalence of bTB is likely to increase, as cross-bred cattle are more susceptible to bTB than indigenous cattle [20, 56].

This study revealed variability in bTB prevalence across different subgroups such as the year of study, diagnostic test used, and geographical districts. Studies conducted before 2015 reported a higher prevalence (9%) compared to those after 2015 (7%). Although this observed discrepancy was not statistically significant, it prompts further discussion and consideration of potential underlying factors contributing to this temporal shift. One plausible explanation for the observed difference in prevalence could be attributed to the transition from the CCT test to the SICTT diagnostics. It is well-documented [31–32] that the SICTT test often yields lower prevalence estimates compared to the traditional CCT test due to its higher specificity. This transition in diagnostic methodologies could have influenced the reported prevalence, since

studies conducted post-2015 predominantly utilized the SICTT test which might explain lower overall prevalence estimates. Furthermore, an increased awareness and consciousness among farmers regarding bTB might be an explanation for lower prevalence estimates in this latter period. It is plausible that increased awareness campaigns, coupled with improved veterinary services and education initiatives, might have led to enhanced disease surveillance and early detection practices. This could result in the culling of infected animals before they reach the advanced stages of the disease, consequently reducing the prevalence observed in more recent studies.

The use of different diagnostic tests produced different results; for instance, CFT indicated a prevalence of 7%, SICTT 6%, and bTB test kits 11%. Methods such as PCR and ELISA showed a prevalence of 9% (Supplementary Figure S2). The use of rapid test kits also showed high prevalence, likely due to their high sensitivity and low specificity [57] (Supplementary Figure S1). Ruling out false positive reactors is unlikely unless an additional ancillary test is employed

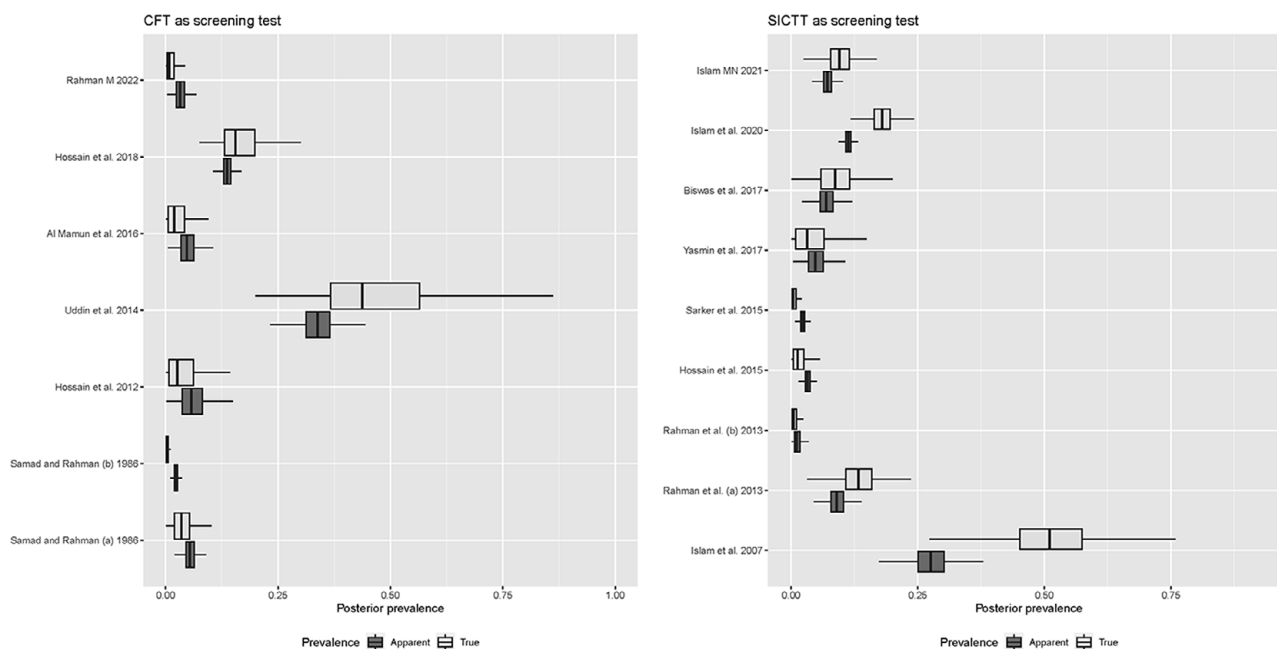


Figure 4. Comparison of bTB apparent and true prevalences through Bayesian Beta-binomial hierarchical models and the use of tPRiors on Caudal Fold Test (CFT) and Single Intradermal Comparative Tuberculin Test (SICTT) in a meta-analysis of bovine tuberculosis in Bangladesh, 1970 to 2023.

[58]. The findings suggest that current diagnostic practices in Bangladesh, primarily using CFT and SICCT as screening tests, might not provide an accurate estimate of the bTB burden. Therefore, unexpected results obtained from these studies might not reflect the actual bTB prevalence in the country. The tuberculin skin tests (such as the SICTT) have limitations in terms of both sensitivity and specificity [28, 59]. To overcome these limitations and enhance diagnostic accuracy, ancillary tests such as the interferon-gamma (IFN- γ) assay should be routinely employed for diagnosis of cattle TB in Bangladesh [59]. To ensure accurate diagnosis and surveillance, better diagnostic tools and supplemental testing methods might be needed.

At the district level, Dhaka, Mymensingh, Sirajganj, Chattogram, and Bhola had a prevalence of 7%, 6%, 8%, 10%, and 3%, respectively. The significantly high prevalence of 34% in Rangpur highlights the need for a location-specific approach to bTB control, considering unique regional factors that may influence disease spread (Supplementary Figure S3). The reason for the high prevalence of bTB in Rangpur is not known. The authors conducted a study involving 150 cattle across five large dairy herds, with herd sizes ranging from 212 to 467 [43]. However, the selection criteria for sampling were not explicitly reported in the published study. Indeed, if the study selectively sampled cattle suspected of having TB, it would likely increase the prevalence estimated. In addition, this study used CFT for screening, which is known to have higher sensitivity but lower specificity compared to SICTT.

The findings of this meta-analysis reveal an important difference between the true prevalence of bTB and the apparent prevalence estimated in the studies included. The true prevalence, when adjusted for test inaccuracies using Bayesian hierarchical beta-binomial models with tPRiors, deviated from the apparent prevalence. This underscores the critical importance of accounting for the accuracy of diagnostic tests when determining bTB prevalence.

This discrepancy emphasizes the importance of considering the sensitivity and specificity of the diagnostic applied tests when estimating the prevalence of bTB. If a diagnostic test has high sensitivity but low specificity, it might identify more true positives but also a high proportion of false positive reactors. In contrast, a test with high specificity but low sensitivity may correctly identify more true negatives but also a high proportion of false negative reactors. The difference between the 'true' prevalence and the apparent prevalence, after correcting for misclassification bias, also relies on the initial apparent prevalence. This pattern is evident in Figure 4 where the impact of correcting for false negatives becomes less significant than the impact of correcting for false positives in studies with few observed positives. This misclassification bias can significantly impact the estimated prevalence and may lead to an underestimation of the true burden of bTB in the population.

Limitations

This meta-analysis has certain limitations. One limitation of our meta-analysis is the lack of studies with representative samples covering a wide geographical range in Bangladesh. This might have caused an incomplete representation of the true bTB prevalence in Bangladesh. Furthermore, research has highlighted discrepancies in the quality, origin, and source of tuberculin used in the tuberculin skin test (TST), indicating a lack of uniformity [60]. Moreover, variability in tests – including differences in sensitivity and specificity of tuberculin-based methods – can introduce heterogeneity in prevalence estimates [61, 62]. The varying performance and discrepancies observed in current diagnostic tests highlight the need for a more uniform and standardized approach. To address these limitations and improve the accuracy of bTB prevalence estimation in Bangladesh, the implementation of a country-wide surveillance programme is essential.

Such a programme should utilize a single, standardized, and validated TST following World Organization for Animal Health (WOAH)-approved methods, using purified protein derivatives (PPDs). By adopting a standardized and comprehensive approach to surveillance, more reliable data can be generated, aiding in the development of effective strategies for bTB control and prevention in Bangladesh.

Conclusion

The study reported significant variability in TB prevalence estimates in different areas of Bangladesh, indicating varying TB burdens. Therefore, targeted interventions are recommended in districts with higher prevalence to effectively reduce the TB burden and prioritize resource allocation for control measures. The current diagnostic practices in Bangladesh – primarily using CFT and SICCT as screening tests – might not provide an accurate estimate of the impact of bTB. To ensure accurate diagnosis and surveillance, better diagnostic tools and supplemental testing methods might be needed. Furthermore, given the potential underestimation of the true bTB prevalence, there is an urgent need for comprehensive and accurate data collection, including targeted sampling and testing. Within the framework of a potential control or surveillance programme, it is essential to adjust for the sensitivity and specificity of the imperfect diagnostic process for bTB to derive reliable bTB prevalence estimates, which in turn will guide informed decision-making in TB control strategies.

Supplementary material. The supplementary material for this article can be found at <http://doi.org/10.1017/S0950268824001328>.

Data availability statement. The data generated during the review process is included in the manuscript and its associated supplementary files.

Author contribution. Conceptualization: S. S.I, A. K. M. A. R.; Methodology: S. S.I., A. K. M. A. R.; Formal analysis: K. P., P. K.; Data Curation: S. S.I, A. K. M. A. R.; Investigation: S. S.I., S. M.L.K.; Writing – S. S.I, A. K. M. A. R, M.P.W.; Writing – Review & Editing: K. P., P. K, M.L.K., M.P.W., and Supervision: S. S.I., S. M.L.K All the authors have read and approved the manuscript for submission in this journal.

Funding statement. No financial assistance was necessary for the execution of this research.

Competing interest. The authors declare that they have no known competing financial interests or personal associations that might be perceived as influencing the findings presented in this paper.

Ethical standard. The authors confirm their adherence to the ethical guidelines outlined on the journal's author guidelines page. They further clarify that ethical approval was not obligatory for this review article, as it does not contain any original research data.

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